

FIG. 1

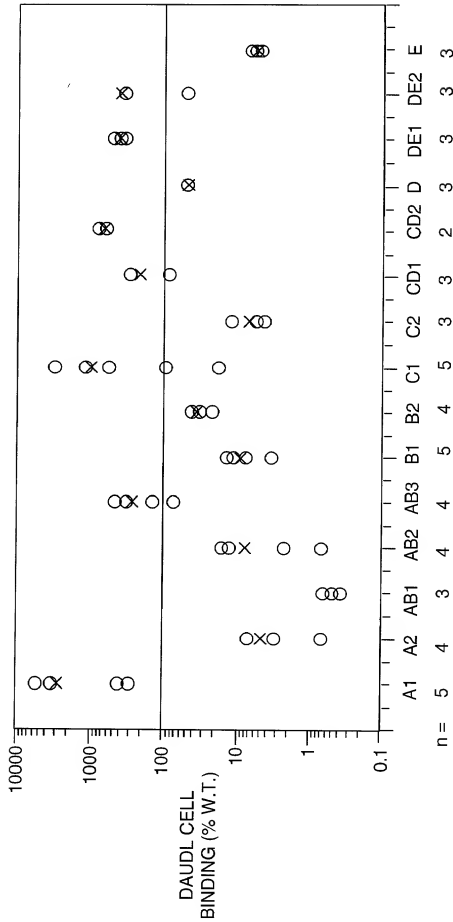


FIG. 2

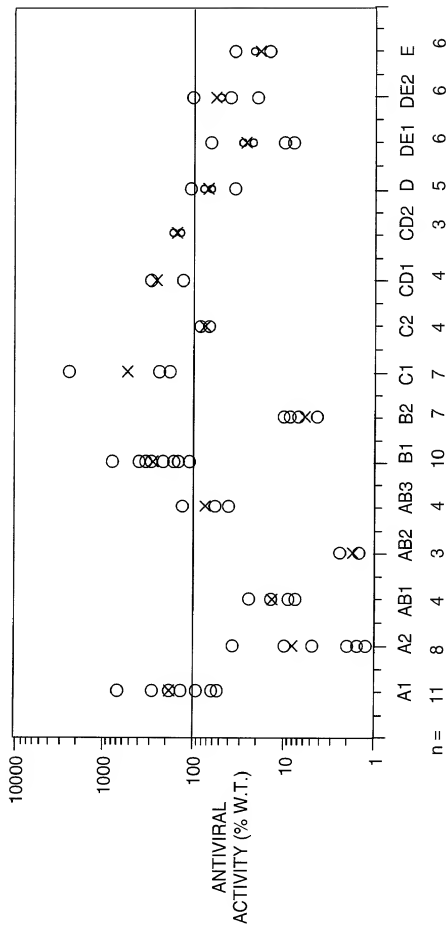


FIG. 3

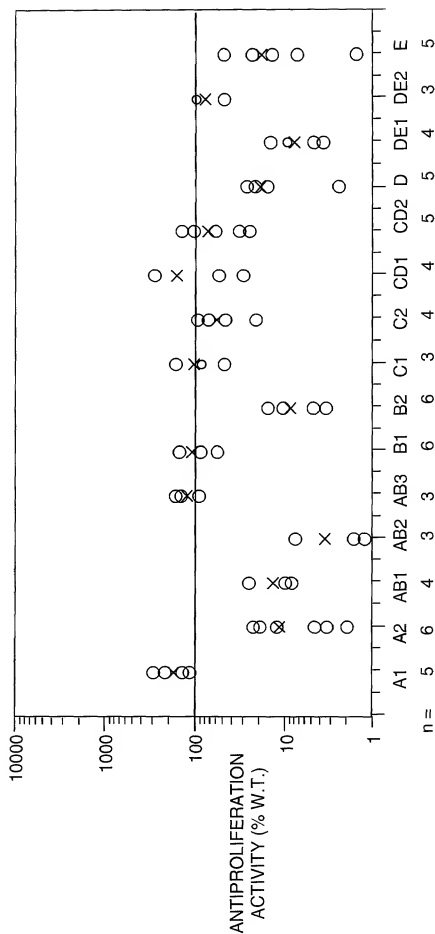


FIG. 4

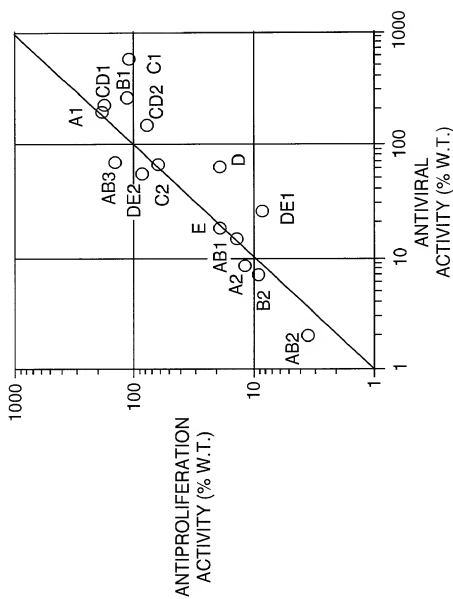


FIG. 5

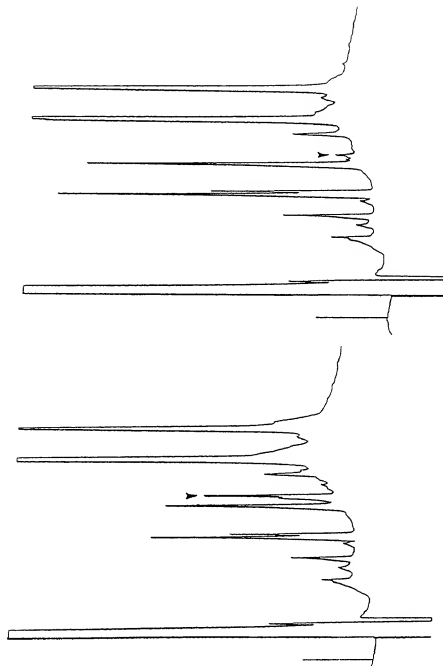


FIG. 6A

FIG. 6B

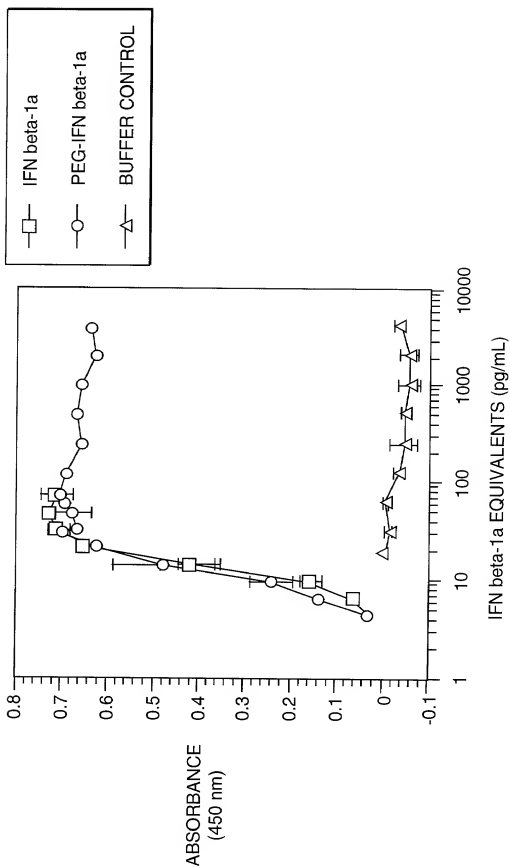


FIG. 7

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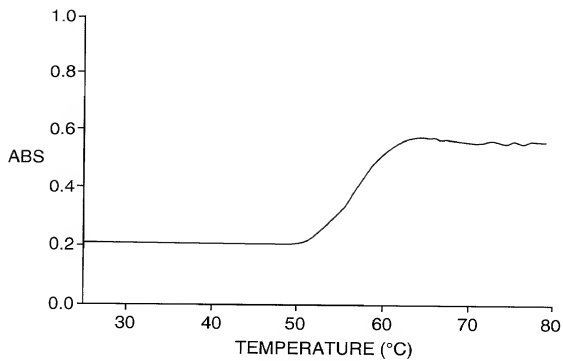


FIG. 8a

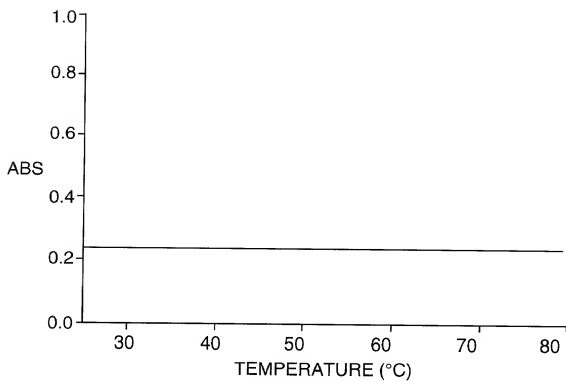


FIG. 8b



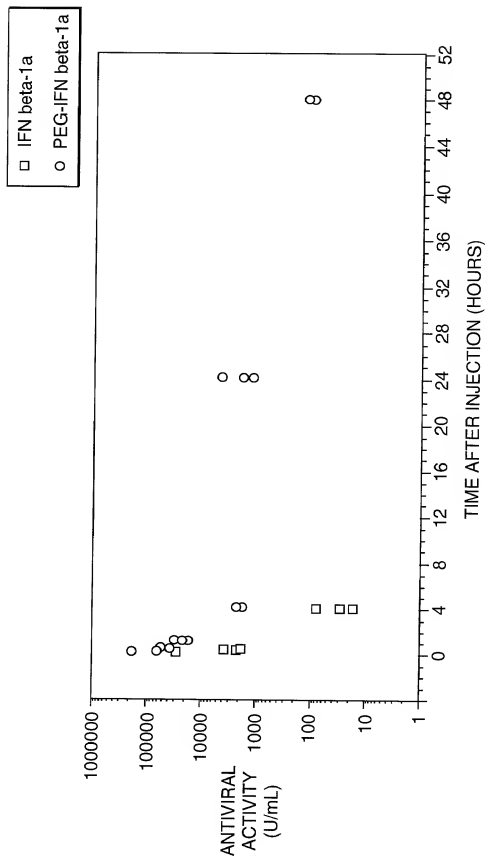


FIG. 9

1 TCCGGGGGCC ATCATCATCA TCATCATAGC TCCGGAGACG ATGATGACAA GATGAGCTAC  
 AGGCCCCCGG TAGTAGTAGT AGTAGTATCG AGGCCTCTGC TACTACTGTT CTACTCGATT  
 1 Ser Gly y Gly i s Hi s Hi s Ser Ser Gly Asp A s p Asp Asp Ly s Met Ser Tyr  
 61 AACTTGCTTG GATTCTACA AAGAAGCAGC AATTTTCAGT GTCAGAAGCT CCTGTGGCAA  
 TTGAACGAAC CTAAGGATGT TTCTTCGTCG TTAAGAGTCA CAGTCTTCGA GGACACCGTT  
 21 Asn Leu Leu G ly Phe Leu Gl n Ar g Ser Ser Asn Phe Gl n C ys Gl n Lys Le u Leu Trp Gl n  
 121 TTGAATGGGA GGCTTGAATA CTGCCTCAAG GACAGGATGA ACTTTGACAT CCCTGAGGAG  
 AACTTACCCT CCGAAGTTAT GACGGAGTTC CTGTCCTACT TGAAGCTGTA GGGACTCCTC  
 41 Leu Asn Gly A r g Leu Gl u Ty r Cys Leu Lys Asp Ar g Met A s n Phe As p I l e Pr o Gl u Gl u  
 181 ATTAAGCAGC TGCAGCAGTT CCAGAAGGAG GACGCCGAT TGACCATCTA TGAGATGCTC  
 TAATTCTGTC ACCTCGTCAA GGTCTTCCTC CTGCGGCGTA ACTGGTAGAT ACTCTACGAG  
 61 I l e Lys Gl n L eu Gl n Gl n Ph e Gl n Lys Gl u Asp Al a Al a L eu Thr l l e Ty r Gl u Met Leu  
 241 CAGAACATCT TTGCTATTTT CAGACAAGAT TCATCTAGCA CTGGCTGGAA TGAGACTATT  
 GTCTTTGAGA AACGATAAAA GTCTGTTCTA AGTAGATCGT GACCGACCTT ACTCTGATAA  
 81 Gl n Asn l l e P he Al a l l e Ph e Ar g Gl n Asp Ser Ser Ser T hr Gl y Tr p As n n Gl u Thr l l e  
 301 GTTGAGAACC TCCTGGCTAA TGTCTATCAT CAGATAAACC ATCTGAAGAC AGTCCTGGAA  
 CAACTCTTGG AGGACCGATT ACAGATAGTA GTCTATTTGG TAGACTTCTG TCAGGACCTT  
 101 Val Gl u Asn L eu Leu Al a As n Val Tyr Hi s Gl n l l e Asn H i s Leu Lys Th r Val Leu Gl u  
 361 GAAAACTGG AGAAAGAAGA TTTCAACAGG GAAAACTCA TGAGCAGTCT GCACCTGAAA  
 CTTTTTGACC TCTTTCTTCT AAAGTGGTCC CCTTTTGAGT ACTCGTCAGA CGTGGACTTT  
 121 Gl u Lys Leu G l u Lys Gl u As p Phe Thr Ar g Gl y Lys Leu M et Ser Ser Le u Hi s Leu Lys  
 421 AGATATTATG GGAGGATTCT GCATTACCTG AAGGCCAAGG AGTACAGTCA CTGTGCCTGG  
 TCTATAATAC CCTCCTAAGA CGTAATGGAC TTCGGTTTCC TCATGTCAGT GACACGGACC  
 141 Ar g Tyr Tyr G ly Ar g l l e Le u Hi s Tyr Leu Lys Al a Lys G l u Tyr Ser Hi s Cys Al a Trp  
 481 ACCATAGTCA GAGTGGAAAT CCTAAGGAAC TTTTACTTCA TTAACAGACT TACAGGTTAC  
 TGGTATCAGT CTCACCTTTA GGATTCCTTG AAAATGAAGT AATTGTCTGA ATGTCCAATG  
 161 Thr l l e Val A r g Val Gl u l l e Leu Ar g Asn Phe Tyr Phe l e Asn Ar g Le u Thr Gl y Tyr  
 541 CTCCGAAC  
 GAGGCTTTG  
 181 Leu Ar g Asn

FIG. 10

